

Abstract

Methods are disclosed for fast and accurate readout of kidney toxicity before it occurs and before it is demonstrated by histopathology examination. Ultimately, this approach shall allow earlier compound selection. The twelve genes identified, namely Calbindin-D28k, KIM-1, OPN, EGF, Clusterin, VEGF, OAT-K1, Aldolase A, Aldolase B, Podocin, Alpha-2u and C4, were grouped and ultimately can be assessed in the form of a kit using PCR, a high throughput technology, in order to characterize and rank new compounds according to their anticipated general kidney toxicity. Also disclosed are methods for identifying agents useful in the treatment of kidney disease, methods for monitoring the efficacy of a treatment for kidney disease and kidney-specific vectors including the sequences of the disclosed genes, and a method for identifying a candidate gene associated with a biological process including kidney function.